

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:52:29 ; Search time 39.52 Seconds
(without alignments)
34.695 Million cell updates/sec

Title: US-09-822-110-36
Perfect score: 91
Sequence: 1 EIKAKRHDEQRELEEE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 75%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_68:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
------------	-------------	--------	----	-------------

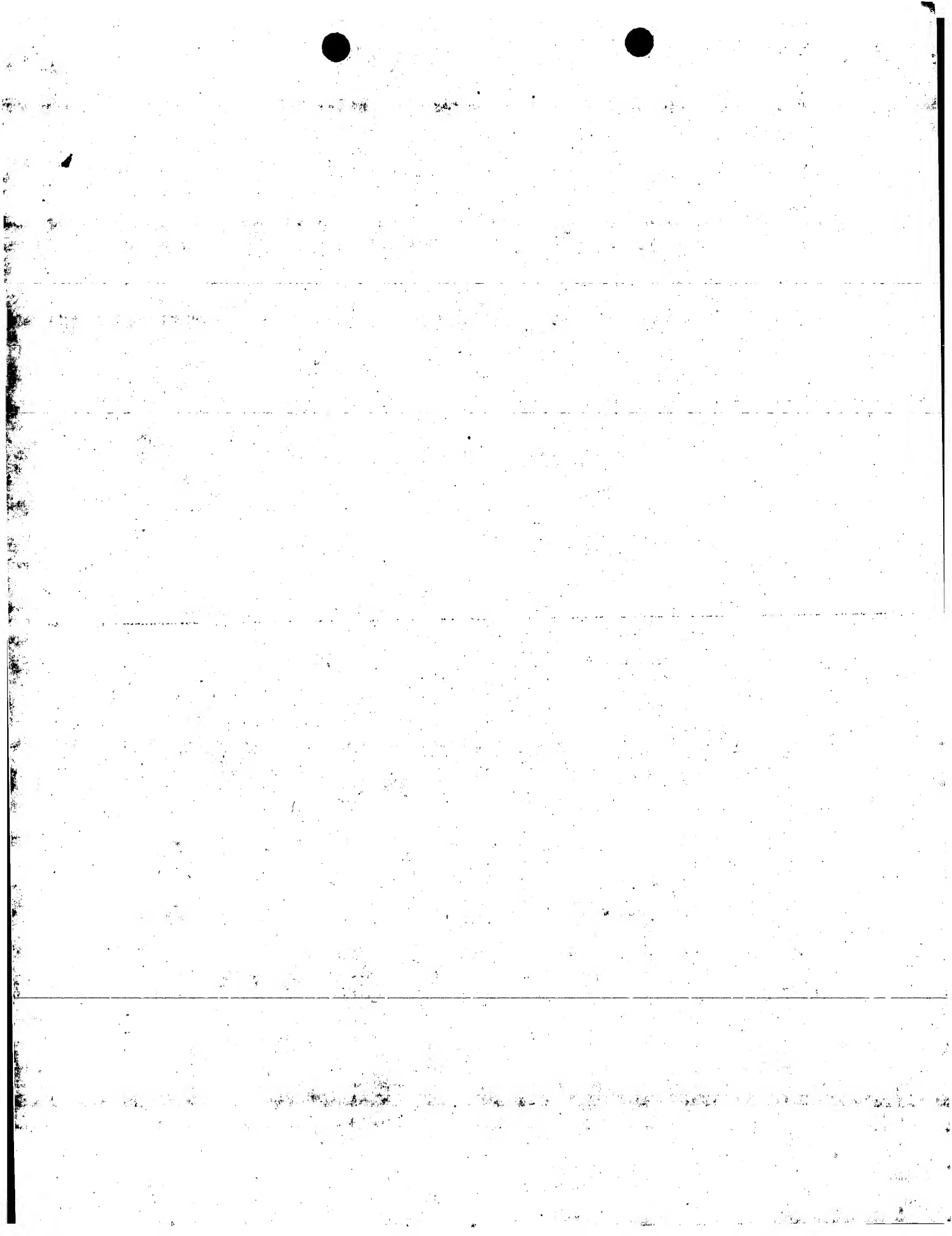
No matches found

Search completed: March 1, 2002, 13:53:17,
Job time: 48 sec

"Newly identified stress-responsive protein kinases, Krs-1 and Krs-RT

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Search completed: March 1, 2002, 13:59:14
Job time: 400 sec
```

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Search completed: March 1, 2002, 13:59:14
Job time: 400 sec
```



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:52:29 ; Search time 63.1 Seconds
(without alignments)
41.726 Million cell updates/sec

Title: US-09-822-110-36
Perfect score: 91
Sequence: 1 EIKAKRHDEQORELEEE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 75%
Maximum Match 100%

Listing first: 50 summaries

Database :
1: SPREMBL_17:*
2: SP_archaea:*
3: SP_bacteria:*
4: SP_fungi:*
5: SP_human:*
6: SP_invertebrate:*
7: SP_mammal:*
8: SP_mhcc:*
9: SP_organelle:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	95.6	321	11	Q9CWM82 mus musculus
2	87	95.6	445	11	Q60877 mus musculus
3	87	95.6	497	11	Q9J110 mus musculus
4	84	92.3	491	11	O54748 rat mus norv

ALIGNMENTS

RESULT 1
ID Q9CWM82 PRELIMINARY: PRT: 321 AA.
AC Q9CWM82;
DT 01-JUN-2001 (TREMBLER, 17, Created)
DT 01-JUN-2001 (TREMBLER, 17, Last sequence update)
DT 01-JUN-2001 (TREMBLER, 17, Last annotation update)
DE 0610042106RIK PROTEIN (FRAGMENT).
GN 0610042106RIK.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinaagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kusakawa T., Saito R.,
RA Kaota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK002914; BAB22453.1;
DR MGD: MGI:1914102; 0610042106rik.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
FT
FT NON_TER
SQ
SEQUENCE 321 AA; 37201 MW; 2E96FD4E919F53A4 CRC64;
Query Match 95.6%; Score 87; DB 11; Length 321;
Best Local Similarity 94.4%; Pred. No. 0.00054;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIKAKRHDEQORELEEE 18
Db 120 EIKAKRHDEQORELEEE 137
RESULT 2
ID Q60877 PRELIMINARY: PRT: 445 AA.
AC Q60877;
DT 01-NOV-1996 (TREMBLER, 01, Created)
DT 01-NOV-1996 (TREMBLER, 01, Last sequence update)
DT 01-JUN-2001 (TREMBLER, 17, Last annotation update)
DE PROTEIN KINASE MESSI.
GN STK3 OR MESS1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RL Han J.,
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U28726; AAA75300.1;
DR HSSP: P00518; 1PHK.
DR MCD: MGI:1928487; SLK3.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00220; S_TKC; 1.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 445 AA; 50407 MW; 7B936B28DA616F05 CRC64;

Query Match
Best Local Similarity 95.6%; Score 87; DB 11; Length 445;
Pred. No. 0.00072;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EIKAKRHDEQORELEEE 18
DB 296 EIKAKRHDEQORELEEE 313

RESULT 3
O9J10 PRELIMINARY; PRT; 497 AA.

DR 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE STE20-LIKE KINASE MST2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Lee K.-K.; Ohyama T.; Yajima N.; Yonehara S.;
RT "MST, a physiological caspase substrate, highly sensitizes apoptosis
both upstream and downstream of caspase activation."
RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF271361; AAF57590.1;
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 497 AA; 56655 MW; 9CDD365437581665 CRC64;

Query Match
Best Local Similarity 95.6%; Score 87; DB 11; Length 497;
Pred. No. 0.00079;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EIKAKRHDEQORELEEE 18
DB 296 EIKAKRHDEQORELEEE 313

RESULT 4
O54748 PRELIMINARY; PRT; 491 AA.

AC 054748;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MST2 KINASE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Aurisicchio L.; Dilauro R.; Zannini M.;
RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ001529; CAA04814.1;

DR HSSP: P00518; IPHK.
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 491 AA; 56121 MW; 90FA6B020E7FFD62 CRC64;

Query Match
Best Local Similarity 92.3%; Score 84; DB 11; Length 491;
Pred. No. 0.0019;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EIKAKRHDEQORELEEE 18
DB 296 EIKAKRHDEQORELEEE 313

Search completed: March 1, 2002, 14:00:24
Job time: 475 sec

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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:52:29 ; Search time 99.08 Seconds
(without alignments)
13.457 Million cell updates/sec

Title: US-09-822-110-36
Perfect score: 91
Sequence: 1 EIKAKRHDEQRELEEE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 75%
Maximum Match 100%
Listing first 50 summaries

Database : A_Geneseq_1101.*
1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
10: /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*
11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*
13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*
15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*
16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*
17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*
18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*
19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: March 1, 2002, 13:55:55
Job time: 206 sec

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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:52:29 ; Search time 45.38 Seconds
(without alignments)
8.926 Million cell updates/sec

Title: US-09-822-110-36
Perfect score: 91
Sequence: I EIKAKRHDEQORELEEE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 75%
Maximum Match 100%
Listing first 50 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

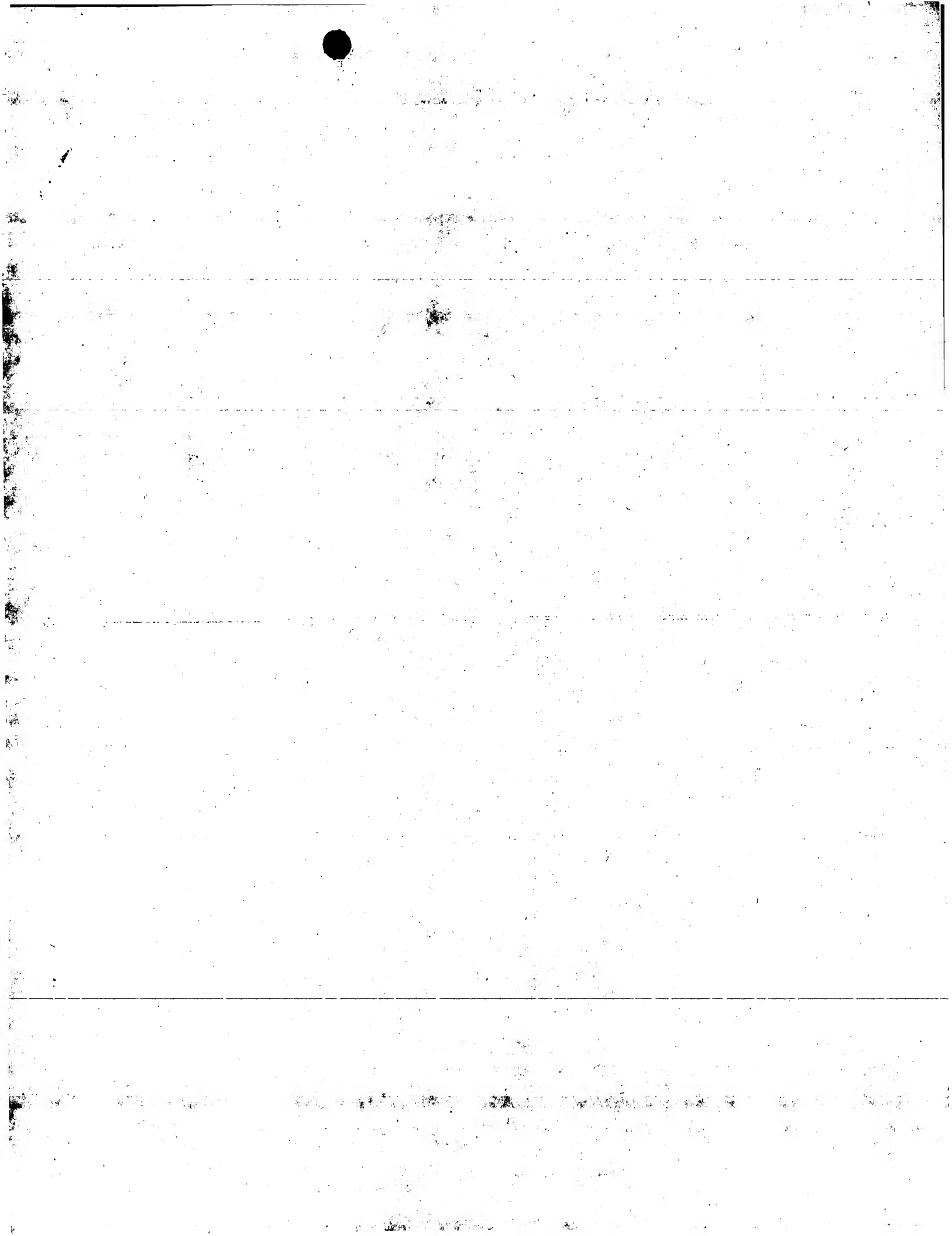
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
------------	-------	--------------------	----	-------------

No matches found

Search completed: March 1, 2002, 13:54:09
db time: 100 sec



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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:53:17 ; Search time 39.52 seconds
(without alignments)
30.840 Million cell updates/sec

Title: US-09-822-110-50

Perfect score: 84
Sequence: 1 EEEENSDDELDST 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 75%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_68:*
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
------------	-------------	-------	--------	----	-------------

No matches found

Search completed: March 1, 2002, 13:53:17
Run time: 48 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:59:14 ; Search time 21.69 Seconds
(without alignments)
27.046 Million cell updates/sec

Title: US-09-822-110-50

Perfect score: 84

Sequence: 1 EEEENSDEDELSHT 16

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 segs, 36664827 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 75%

Maximum Match 100%

Listing first 50 summaries

Database : SwissProt_39:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	ID	Description
1	84	100.0	491 1	STE20-LIKE KINASE 2 (STE20-LIKE KINASE 2)

ALIGNMENTS

RESULT 1
ID STE20-LIKE KINASE 2 (STE20-LIKE KINASE 2)
Q13188: Q13188.1 (STE20-LIKE KINASE 2)
20-AUG-2001 (Rel. 40, last sequence update)
20-AUG-2001 (Rel. 40, last sequence update)
20-AUG-2001 (Rel. 40, last sequence update)
SERINE/THREONINE PROTEIN KINASE 3 (EC 2.7.1.37) (STE20-LIKE KINASE 2)
DE (SERINE/THREONINE PROTEIN KINASE 3)
DE (SERINE/THREONINE PROTEIN KINASE 3)
GN STE20-LIKE KINASE 2
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN NM_001001001.1
RP SEQUENCE FROM N.A.
RX MEDLINE=96144292; PubMed=8566796;
RA "Cloning and characterization of a member of the MST subfamily of Ste20-like kinases."
RT Ste20-Like Kinases
RL Gene 167:303-306(1995).
RN NM_001001001.1
RP SEQUENCE FROM N.A.
RX MEDLINE=96413604; PubMed=8816758;
RA Taylor L.K., Wang H.C., Erikson R.L.
RT Newly identified stress-responsive protein kinases, Krs-1 and Krs-2.

2. "Proc. Natl. Acad. Sci. U.S.A. 93:10099-10104(1996).
[3] SEQUENCE OF 96-203 FROM N.A.
RX MEDLINE=94100173; PubMed=8274451;
RA Schultz S.J., Nigg E.A.;
RT "Identification of 21 novel human protein kinases, including 3 members of a family related to the cell cycle regulator nimA of Aspergillus nidulans."
RL Cell Growth Differ. 4:821-830(1993).
CC -1- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN -> ADP + A PHOSPHOPROTEIN.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN ADULT KIDNEY, SKELETAL AND PLACENTA TISSUES AND AT VERY LOW LEVELS IN ADULT HEART, LUNG AND BRAIN TISSUES.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. STE20 SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).
CC -----
DR EMBL: U26424; AAC50386.1;
DR EMBL: U60206; AAB17261.1;
DR EMBL: Z25422; CAA80909.1;
DR HSSP: P00518; 1PK.
DR MIM: 605030;
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; PKinase_1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; STKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR TRANSFERASE: Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 27 278
FT NP_BIND 33 41
FT BINDING 56 56
FT ACT_SITE 146 146
FT DOMAIN 308 314
FT DOMAIN 370 375
FT CONFLICT 96 98
FT CONFLICT 121 121
FT CONFLICT 203 203
FT CONFLICT 303 303
FT CONFLICT 332 334
FT SEQUENCE 491 AA; 56261 MW; 9CA3B0644F3C14A9 CRC64;
Query Match 100.0%; Score 84; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EEEENSDEDELSHT 16
DB 310 EEEENSDEDELSHT 325
Search completed: March 1, 2002, 13:59:14
Job time: 400 sec

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OM protein - protein search, using sw model

Run on: March 1, 2002, 14:00:24 ; Search time 63.1 Seconds
(without alignments)
37.090 Million cell updates/sec

Title: US-09-822-110-50

Perfect score: 84
Sequence: 1 EEEENSDEDELDSHT 16

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 75%
Maximum Match 100%
Listing first 50 summaries

Database: 1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mnc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

suit	No.	Score	Query	Match	Length	ID	Description
1	84	100.0	321	11	09CW82	09CW82 mus musculu	
2	84	100.0	445	11	060877	060877 mus musculu	
3	84	100.0	497	11	09J110	09J110 mus musculu	
4	81	96.4	491	11	054748	054748 rattus norv	

ALIGNMENTS

RESULT 1
09CW82 PRELIMINARY: PRT: 321 AA.
AC 09CW82;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 0610042106RIK PROTEIN (FRAGMENT).
GN 0610042106RIK.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
EX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK002914; BAB2453.1;
DR MGD: MGI:1914102; 0610042106RIK.
DR InterPro: IPR000719; Euk-Pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
FT NON_TER
SQ SEQUENCE 321 AA; 37201 MW; 2E96FD4E919F5344 CRC64;

Query Match 100.0%; Score 84; DB 11; Length 321;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 EEEENSDEDELDSHT 16
DB 134 EEEENSDEDELDSHT 149
RESULT 2
060877 PRELIMINARY: PRT: 445 AA.
AC 060877;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PROTEIN KINASE MESSI.
GN STK3 OR MESSI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Han J.,
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U28726; AAA75300.1;
DR HSSP: P00518; IPHK.
DR MGD: MGI:1928487; STK3.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKc; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 445 AA; 50407 MW; 7B936B28DA616F05 CRC64;

Query Match
Best Local Similarity 100.0%; Score 84; DB 11; Length 445;
Pred. No. 0.00014;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEEENSDEDELDST 16
DB 310 EEEENSDEDELDST 325

RESULT 3

OJ0110 PRELIMINARY; PRT; 497 AA.

AC 09J0110; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE STE20-LIKE KINASE MST2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Lee K.-K., Ohnaka T., Yajima N., Yonehara S.;
RT "MST, a physiological caspase substrate, highly sensitizes apoptosis
both upstream and downstream of caspase activation."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF271361; AAF75790.1;
DR InterPro: IPR000719; Euk.pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 497 AA; 56855 MW; 9CDD365437581665 CRC64;

Query Match
Best Local Similarity 100.0%; Score 84; DB 11; Length 497;
Pred. No. 0.00016;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEEENSDEDELDST 16
DB 310 EEEENSDEDELDST 325

RESULT 4

O54748 PRELIMINARY; PRT; 491 AA.

AC 054748; 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE MST2 KINASE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Aurilio L., Dilauro R., Zannini M.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ001529; CAA04814.1;

DR HSP; P00518; IPHK.
DR InterPro: IPR000719; Euk.pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 491 AA; 56121 MW; 90FAB020E7FFD52 CRC64;

Query Match
Best Local Similarity 96.4%; Score 81; DB 11; Length 491;
Pred. No. 0.00043;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEEENSDEDELDST 16
DB 310 EEEENSDEDELDST 325

Search completed: March 1, 2002, 14:00:24
Job time: 475 sec

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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:55:55 ; Search time 99.08 Seconds
(without alignments)
11.962 Million cell updates/sec

Title: US-09-822-110-50

Perfect score: 84
Sequence: 1 EEEENSDDELDLSDHT 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 segs, 74073290 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 75%
Maximum Match 100%
Listing first 50 summaries

Database : A_Geneseq_1101:*

- 1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
No matches found						

Search completed: March 1, 2002, 13:55:55
Job time: 206 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:54:09 ; Search time 45.38 Seconds
(without alignments)
7.934 Million cell updates/sec

Title: US-09-822-110-50

Perfect score: 84
Sequence: 1 EEEBENSDELDLSHT 16

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 75%
Maximum Match 100%
Listing first 50 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfills1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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No matches found

Search completed: March 1, 2002, 13:54:09
Search time: 100 sec

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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:53:17 ; Search time 39.52 Seconds
(without alignments)
65.535 Million cell updates/sec

Title: US-09-822-110-51

Perfect score: 173
Sequence: 1 AMEIKAKRRHDECOARELEEEENSEDELDLSDHTMV 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 segs, 76174552 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 75%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_68:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

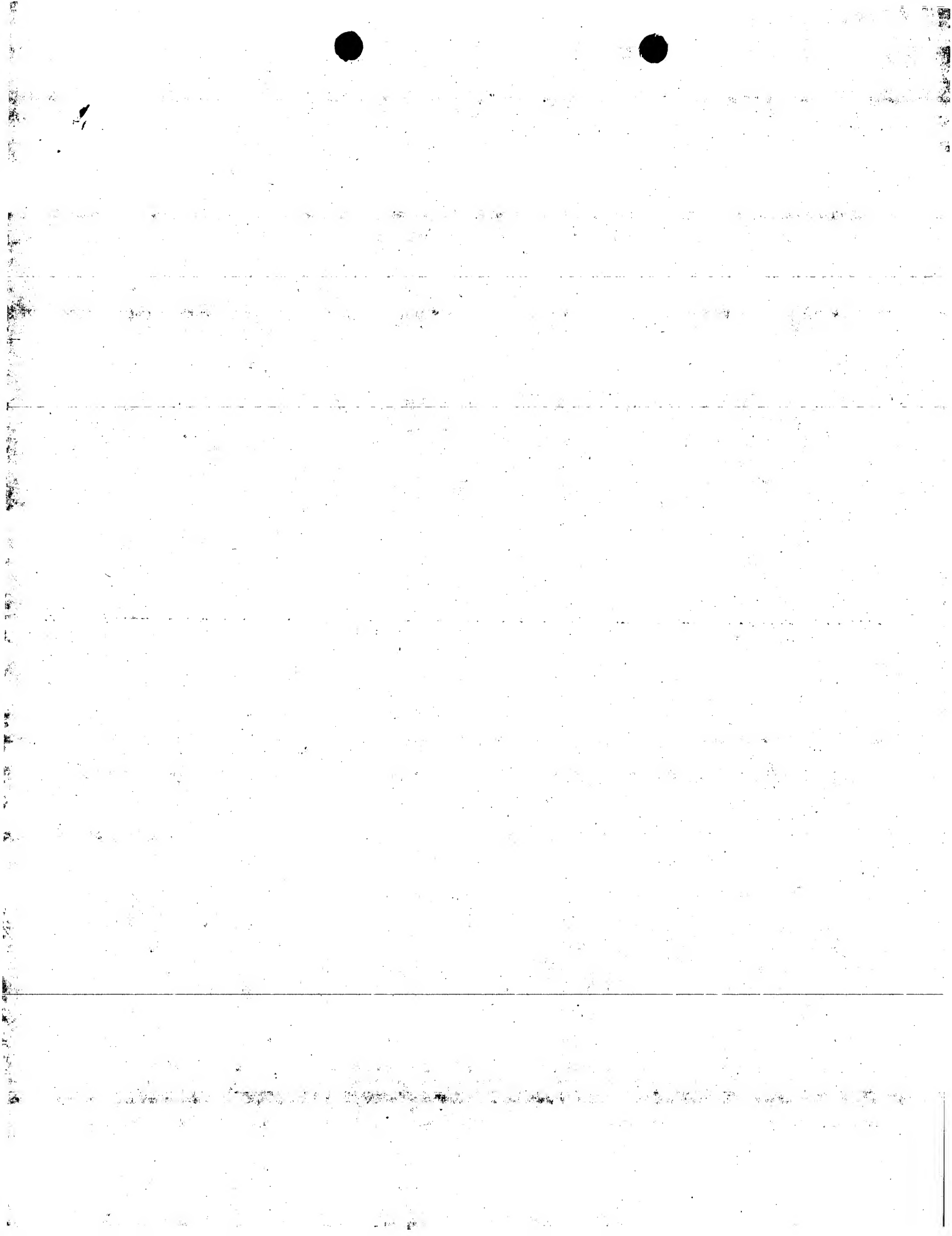
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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No matches found

Search completed: March 1, 2002, 13:53:17
Search time: 48 sec



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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:59:14 ; Search time 21.69 Seconds
(without alignments)
57.474 Million cell updates/sec

Title: US-09-822-110-51

Perfect score: 173

Sequence: 1 AMEIKAKRHDEQORELEEEENSDELDSDHTMV 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 75%

Maximum Match 100%

Listing first 50 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	173	100.0	491	1	STK3_HUMAN

ALIGNMENTS

RESULT 1	STK3_HUMAN	STANDARD:	PRT:	491 AA.
ID	STK3_HUMAN	Q13188; Q15801; Q15445;		
DT	20-AUG-2001 (Rel. 40, Last sequence update)			
DE	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	STE20-LIKE KINASE 3 (EC 2.7.1.37) (STE20-LIKE KINASE 2)			
DE	(SERINE/THREONINE PROTEIN KINASE KRS-1).			
GN	STK3 OR MST2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96144292; PubMed=8566796;			
RA	Creasy C.L., Chernoff J.;			
RT	"Cloning and characterization of a member of the MST subfamily of			
RT	Ste20-like kinases."			
RL	Gene 167:303-306(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96413604; PubMed=8816758;			
RA	Taylor L.K., Wang H.C., Erikson R.L.;			
RT	"Newly identified stress-responsive protein kinases, Krs-1 and Krs-			

RT	2.	Proc. Natl. Acad. Sci. U.S.A. 93:10099-10104(1996).
RL	[3]	
RP	SEQUENCE OF 96-203 FROM N.A.	
RX	MEDLINE=94100173; PubMed=8274451;	
RA	Schultz S.J., Nigg E.A.;	
RT	"Identification of 21 novel human protein kinases, including 3 members	
RT	of a family related to the cell cycle regulator pima of Aspergillus	
RT	nidulus."	
RL	Cell Growth Differ. 4:821-830(1993).	
CC	-1- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT	
CC	MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS (BY	
CC	SIMILARITY).	
CC	-1- CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN.	
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).	
CC	-1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN ADULT KIDNEY,	
CC	SKELETAL AND PLACENTA TISSUES AND AT VERY LOW LEVELS IN ADULT	
CC	HEART, LUNG AND BRAIN TISSUES.	
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.	
CC	STE20 SUBFAMILY.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@sib-sib.ch).	
CC	-----	
DR	EMBL; U26424; AAC50386.1; -	
DR	EMBL; U60206; AAB17261.1; -	
DR	EMBL; Z25422; CAAB0909.1; -	
DR	HSSP; P00518; IPHK.	
DR	MIM; 605030; -	
DR	InterPro; IPR000719; Euk_Pkinase.	
DR	InterPro; IPR002290; Ser_thr_kin_actsite.	
DR	Pfam; PF00069; Pkinase; 1.	
DR	PRINTS; PRO0109; TYRKINASE.	
DR	SMART; SMO0220; S_TKC; 1.	
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP_1.	
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.	
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.	
DR	Transferase; Serine/threonine-protein kinase; ATP-binding.	
FT	DOMAIN 27 278	
FT	NP_BIND 33 41	
FT	ACT_SITE 56 56	
FT	DOMAIN 146 146	
FT	DOMAIN 308 314	
FT	DOMAIN 370 375	
FT	CONFLICT 96 98	
FT	CONFLICT 121 121	
FT	CONFLICT 121 121	
FT	CONFLICT 203 203	
FT	CONFLICT 303 303	
FT	CONFLICT 332 334	
FT	SEQUENCE 491 AA; 56261 MW; 9CA3B0644F3C1A49 CRC64;	
QY	1 AMEIKAKRHDEQORELEEEENSDELDSDHTMV 34	
DB	294 AMEIKAKRHDEQORELEEEENSDELDSDHTMV 327	
Query Match	100.0%	Score 173; DB 1; Length 491;
Best Local Similarity	100.0%	Pred. No. 2, 1e-10;
Matches 34; Conservative	0; Mismatches	0; Indels 0; Gaps 0;

Search completed: March 1, 2002, 13:59:15
Job time: 401 sec

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OM protein - protein search, using sw model

Run on: March 1, 2002, 14:00:24 ; Search time 63.1 Seconds
(without alignments)
78.816 Million cell updates/sec

Title: US-09-822-110-51

Perfect score: 173

Sequence: 1 AMEIKAKRHDEQORELEEEENSDELDSDHTMV 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 75%

Maximum Match 100%

Listing first 50 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	ID	Description
1	169	97.7	321	11	09CW82 mus muscula
2	169	97.7	445	11	09CW82 mus muscula
3	169	97.7	497	11	09J110 mus muscula
4	162	93.6	491	11	054748 rattus norv

ALIGNMENTS

RESULT 1
09CW82 PRELIMINARY; PRT; 321 AA.
AC 09CW82;
DT 01-JUN-2001 (TREMBLREL, 17, Created)
DT 01-JUN-2001 (TREMBLREL, 17, Last sequence update)
DT 01-JUN-2001 (TREMBLREL, 17, Last annotation update)
DE 0610042106RIK PROTEIN (FRAGMENT).
GN 0610042106RIK.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC SMPRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinaigawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Atakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaudo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill L., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK002914; BAB22453.1;
DR MCD: MGI:1914102; 0610042106RIK.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase.1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
FT NON_TER 1 1
SQ SEQUENCE 321 AA; 37201 MW; 2E96PD4E919F5344 CRC64;

Query Match 97.7%; Score 169; DB 11; Length 321;
Best Local Similarity 97.1%; Pred. No. 5.8e-11;
Matches 33; Conservative 1; Mismatches 0; Gaps 0;
QY 1 AMEIKAKRHDEQORELEEEENSDELDSDHTMV 34
118 AMEIKAKRHDEQORELEEEENSDELDSDHTMV 151
RESULT 2
060877
ID 060877 PRELIMINARY; PRT; 445 AA.
AC 060877;
DT 01-NOV-1996 (TREMBLREL, 01, Created)
DT 01-NOV-1996 (TREMBLREL, 01, Last sequence update)
DT 01-JUN-2001 (TREMBLREL, 17, Last annotation update)
DE PROTEIN KINASE MESSI.
GN STR3 OR MESSI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Han J.,
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U28726; AAA75300.1;
DR HSSP: P00518; IPHK.
DR MCD: MGI:1928487; SLK3.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase.1.
DR SMART: SM00220; S_TKC; 1.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Transferase
 SQ SEQUENCE 445 AA; 50407 MW; 7B936B28DA616F05; CRC64;

Query Match 97.7%; Score 169; DB 11; Length 445;
 Best Local Similarity 97.1%; Pred. No. 7.6e-11;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMEIKARHDEQORELEEEENSDEDELDSHTMV 34
 DB 294 AMEIKARHDEQORELEEEENSDEDELDSHTMV 327

RESULT 3
 09J110 PRELIMINARY; PRT; 497 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE STE20-LIKE KINASE MST2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RA Lee K. K., Ohyama T., Yajima N., Yonehara S.;
 RT "MST, a physiological caspase substrate, highly sensitizes apoptosis
 RT both upstream and downstream of caspase activation."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF271361; AAF75790.1;
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR InterPro: IPR001245; Tyr_kin.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; kinase; transferase.
 SQ SEQUENCE 497 AA; 56855 MW; 9CDD365437581665; CRC64;

Query Match 97.7%; Score 169; DB 11; Length 497;
 Best Local Similarity 97.1%; Pred. No. 8.4e-11;
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMEIKARHDEQORELEEEENSDEDELDSHTMV 34
 DB 294 AMEIKARHDEQORELEEEENSDEDELDSHTMV 327

RESULT 4
 054748 PRELIMINARY; PRT; 491 AA.

AC 054748;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE MST2 KINASE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ausio J., D'Amico R., Zannini M.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ001529; CAA04814.1;

DR HSP: P00518; 1PK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; transferase.
 SQ SEQUENCE 491 AA; 56121 MW; 90FA6B020E7FFD62; CRC64;

Query Match 93.6%; Score 162; DB 11; Length 491;
 Best Local Similarity 93.9%; Pred. No. 4.7e-10;
 Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 MEIKARHDEQORELEEEENSDEDELDSHTMV 34
 DB 295 MEIKARHDEQORELEEEENSDEDELDSHTMV 327

Search completed: March 1, 2002, 14:00:24
 Job time: 475 sec

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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:55:55 ; Search time 99.08 seconds
(without alignments)
25.419 Million cell updates/sec

Title: US-09-822-110-51
Perfect score: 173
Sequence: 1 AMEIKAKRHDEQORELEEEENSDDELDSHTMV 34

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 75%
Maximum Match 100%
Listing first 50 summaries

Database: A_Geneseq_1101.*

- 1: /SID88/gcgcdata/geneseq/AA1980.DAT.*
- 2: /SID88/gcgcdata/geneseq/AA1981.DAT.*
- 3: /SID88/gcgcdata/geneseq/AA1982.DAT.*
- 4: /SID88/gcgcdata/geneseq/AA1983.DAT.*
- 5: /SID88/gcgcdata/geneseq/AA1984.DAT.*
- 6: /SID88/gcgcdata/geneseq/AA1985.DAT.*
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- 8: /SID88/gcgcdata/geneseq/AA1987.DAT.*
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- 11: /SID88/gcgcdata/geneseq/AA1990.DAT.*
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- 20: /SID88/gcgcdata/geneseq/AA1999.DAT.*
- 21: /SID88/gcgcdata/geneseq/AA2000.DAT.*
- 22: /SID88/gcgcdata/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
No matches found					

Search completed: March 1, 2002, 13:55:55
Job time: 206 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:54:09 ; Search time 45.38 Seconds
(without alignments)
16.860 Million cell updates/sec

Title: US-09-822-110-51

Perfect score: 173
Sequence: 1 AMEIKAKRHDEQORELEEEENSDSELDLSHTMV 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 segs, 22503292 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 75%
Maximum Match 100%
Listing first 50 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
------------	-------------	-------	--------	----	-------------

No matches found

rch completed: March 1, 2002, 13:54:09
time: 100 sec

Fri Mar 1 15:20:27 2002

US-09-822-110-58.rpr

Page: 1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:53:17 ; Search time 39.52 Seconds

(Without alignments)
59/752 Million cell updates/sec

Title: US-09-822-110-58

Sequence: 160
1-EIKAKRHDEQOQRELEEEENDEDELDSTHM 31

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 75%
Maximum Match 100%
Listing first 50 summaries

Database :

PIR_68:
1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
------------	-------------	--------	----	-------------

No matches found

Search completed: March 1, 2002, 13:53:17
Search time: 48 sec

20

1. The first of these is the fact that the Government has not yet decided whether it will accept the offer of the United States to purchase the rights in the atomic energy patent. This is a very important question, and it is one which the Government should decide as soon as possible.

1. NAME
 2. ADDRESS
 3. CITY
 4. STATE
 5. ZIP
 6. PHONE
 7. TELETYPE
 8. TELEFAX
 9. TELEVISION
 10. RADIO
 11. MAILING ADDRESS
 12. TELEPHONE
 13. TELETYPE
 14. TELEFAX
 15. TELEVISION
 16. RADIO
 17. MAILING ADDRESS
 18. TELEPHONE
 19. TELETYPE
 20. TELEFAX
 21. TELEVISION
 22. RADIO
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 27. TELEVISION
 28. RADIO
 29. MAILING ADDRESS
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 31. TELETYPE
 32. TELEFAX
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 34. RADIO
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 94. RADIO
 95. MAILING ADDRESS
 96. TELEPHONE
 97. TELETYPE
 98. TELEFAX
 99. TELEVISION
 100. RADIO

[illegible][illegible]

RECEIVED
JUN 13 1964
U.S. DEPARTMENT OF JUSTICE
FEDERAL BUREAU OF INVESTIGATION
WASHINGTON, D.C. 20535

RECEIVED
JUN 10 1968
U.S. DEPARTMENT OF AGRICULTURE
WASHINGTON, D.C.

THE UNIVERSITY OF CHICAGO

[illegible][illegible]

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

Abstract

[The page contains faint, illegible markings.]

[illegible][illegible][illegible]

THE UNIVERSITY OF CHICAGO
CHICAGO, ILLINOIS 60637
U.S.A.
TEL: (312) 937-1234
FAX: (312) 937-1234
E-MAIL: info@uchicago.edu
WWW: <http://www.uchicago.edu>

RECEIVED
JAN 10 1964
U.S. DEPT. OF JUSTICE
FEDERAL BUREAU OF INVESTIGATION
WASHINGTON, D.C. 20535

Q. 3. 30

OFF. 3E.O. 12866-2

100

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OM protein - protein search, using sw model

Run on: March 1, 2002, 14:00:24 ; Search time 63.1 Seconds
(without alignments)
71,861 Million cell updates/sec

Title: US-09-822-110-58

Perfect score: 160
Sequence: 1 EIKAKRHDEQORELEEEENSDDELDSHTM 31

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 75%
Maximum Match 100%
Listing first 50 summaries

Database :
1: SP.TREMBL_17:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp_rodent:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult	No.	Score	Query Match	Length	ID	Description
1	156	97.5	321	11	Q9CW82	mus musculus
2	156	97.5	445	11	Q60877	mus musculus
3	156	97.5	497	11	Q9J110	mus musculus
4	153	95.6	491	11	O54748	rattus norv

ALIGNMENTS

RESULT 1
Q9CW82 PRELIMINARY: PRT: 321 AA.
AC Q9CW82;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 0610042106RIK PROTEIN (FRAGMENT).
GN 0610042106RIK.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamane I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S.J., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK002914; BAB2453.1;
DR MGD: MGI:1914102; 10610042106RIK.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
FT NON_TER 1 1
SQ SEQUENCE 321 AA; 37201 MW; 2E96FDA919F53A4 CRC64;

Query Match 97.5% Score 156; DB 11; Length 321;
Best Local Similarity 96.8%; Pred. NO. 1e-09;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIKAKRHDEQORELEEEENSDDELDSHTM 31
Db 120 EIKAKRHDEQORELEEEENSDDELDSHTM 150
RESULT 2
Q60877 ID 060877 PRELIMINARY: PRT: 445 AA.
AC Q60877;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PROTEIN KINASE MESSI.
GN STK3 OR MESSI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Han J.,
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U28726; AAA75300.1;
DR HSSP: P00518; 1PHK.
DR MGD: MGI:1928487; STK3.
DR InterPro: IPR000719; Ser_thr_kinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKc; 1.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 445 AA; 50407 MW; 7B936B28DA616F05 CRC64;

Query Match 97.5%; Score 156; DB 11; Length 445;
Best Local Similarity 96.8%; Pred. No. 1.3e-09;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EIKARRHDEQORELEEEENSDDELDSHTM 31
DB 296 EIKARRHDEQORELEEEENSDDELDSHTM 326

RESULT 3

O9J110 PRELIMINARY; PRT; 497 AA.
O9J110:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ST20-LIKE KINASE MST2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Lee K.-K., Ohyama T., Yajima N., Yonehara S.;
RT "MST, a physiological caspase substrate, highly sensitizes apoptosis
RT both upstream and downstream of caspase activation."
RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF211361; AAF57590.1;
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_acsite.
DR Pfam: PF00069; TTKINASE.
DR PRINTS: PR00109; TTKINASE.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 497 AA; 56855 MW; 9CDD365437581665 CRC64;

Query Match 97.5%; Score 156; DB 11; Length 497;
Best Local Similarity 96.8%; Pred. No. 1.4e-09;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EIKARRHDEQORELEEEENSDDELDSHTM 31
DB 296 EIKARRHDEQORELEEEENSDDELDSHTM 326

RESULT 4

O54748 PRELIMINARY; PRT; 491 AA.
O54748:
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE MST2 KINASE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Aukisicchio L., Dilauro R., Zannini M.;
RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ001529; CAA04814.1;

DR HSP: P00518; IPHK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_acsite.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 491 AA; 56121 MW; 90FA6B020E7FFD62 CRC64;

Query Match 95.6%; Score 153; DB 11; Length 491;
Best Local Similarity 93.5%; Pred. No. 3e-09;
Matches 29; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EIKARRHDEQORELEEEENSDDELDSHTM 31
DB 296 EIKARRHDEQORELEEEENSDDELDSHTM 326

Search completed: March 1, 2002, 14:00:24
Job time: 475 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:55:55 ; Search time 99.08 Seconds

(without alignments)
23.176 Million cell updates/sec

Title: US-09-822-110-58

Perfect score: 160
Sequence: 1 EIKAKRHDEQORELEEEENSDDELDSHTM 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 segs, 74073290 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 75%
Maximum Match 100%

Listing first 50 summaries

- Database : A_Geneseq_1101.*
- 1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.*
 - 2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
 - 3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.*
 - 4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.*
 - 5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.*
 - 6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.*
 - 7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.*
 - 8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.*
 - 9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.*
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 - 13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.*
 - 14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.*
 - 15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.*
 - 16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.*
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 - 18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.*
 - 19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.*
 - 20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
 - 21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
 - 22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description

No. matches found

Search completed: March 1, 2002, 13:55:55
Job time: 206 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2002, 13:54:09 ; Search time 45.38 Seconds
(without alignments)
15.372 Million cell updates/sec

Title: US-09-822-110-58
Perfect score: 160
Sequence: 1 EIKAKRHDEQCRELEEEENSDDELDSHTM 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 75%
Maximum Match 100%
Listing first 50 summaries

Database :

- Issued_Patents_AA:*
- 1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
 - 2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
 - 3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
 - 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
 - 5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
 - 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
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No. matches found

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